Accepted Manuscript

Title: Performance of a docking/molecular dynamics protocol for virtual screening of nutlin-class inhibitors of Mdmx

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PII: \$1093-3263(16)30470-3

DOI: http://dx.doi.org/doi:10.1016/j.jmgm.2017.02.014

Reference: JMG 6856

To appear in: Journal of Molecular Graphics and Modelling

Received date: 16-12-2016 Revised date: 18-1-2017 Accepted date: 21-2-2017

Please cite this article as: Nagakumar Bharatham, Kristin E.Finch, Jaeki Min, Anand Mayasundari, Michael A.Dyer, R.Kiplin Guy, Donald Bashford, Performance of a docking/molecular dynamics protocol for virtual screening of nutlin-class inhibitors of Mdmx, Journal of Molecular Graphics and Modelling http://dx.doi.org/10.1016/j.jmgm.2017.02.014

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ACCEPTED MANUSCRIPT

Performance of a docking/molecular dynamics protocol for virtual screening of nutlin-class inhibitors of Mdmx

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